

REPLACEMENT SHEET

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Fig. 10

human : G D V E K G K K I F I M K C S Q C H T V E G G K H K T G P N L H G L F G R K SEQ ID NO: 1
bacterium : E G D A A A G E K V S K K C L A C H T F D Q G G A N K V G P N P N L F G V F SEQ ID NO: 2

LCS : G D I x 3 . 3 I G I x 0 . 1 I K I x 0 . 2 I K I x 4 . 0 I K C I x 2 . 2 I C H T I x 3 . 3 I G G I x 2 . 2 I K
G D I x 1 . 4 I E I x 0 . 2 I K I x 0 . 2 I K I x 0 . 4 I K C I x 2 . 2 I C H T I x 3 . 3 I G G I x 2 . 2 I K

homology : 47%

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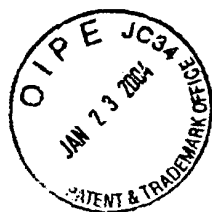
Fig. 11

Rot : MSLAILRVIRLVRVFRIFKLSRHSKGLQILGRTLKASMRELGLIFFIGVV

SEQ ID NO: 3

leucinzip. L (6) L (6) L (6) L (6) L

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Fig. 12

human : G D V E K G K K I F I M K C S Q C H T V E K G G K H K T G P N L H G L F G R K ... SEQ ID NO: 1
bacterium: E G D A A G E K V S K K C L A C H T F D G G A N K V G P N P N L F G V F ... SEQ ID NO: 2

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Fig. 23 A

| | | |
|-----|------------|-------------|
| 1 | TEEQIAEFKE | AFSLFDKDG |
| 21 | GTITTKELGT | VMRSLGQNPT |
| 41 | EAELQDMINE | VDADGNGTID |
| 61 | FPEFLTMMAR | KMKDTSDEE |
| 81 | IREAFRVFDK | DGNGYISAAE |
| 101 | LRHVMTNLGE | KLTDDEEVDEM |
| 121 | IREANIDGDG | QVNYEEFVQM |
| 141 | MTA | |

AMINO ACID SEQUENCE OF CALMODULIN
(EXCERPT FROM PDB)

SEQ ID NO: 4

Fig. 23 B

| | | |
|-----|------------|-------------|
| 1 | AMDQQAEARA | FLSEEMIAEF |
| 21 | KAAFDMFDAD | GGGDI STKEL |
| 41 | GTVMRMLGQN | PTKEELD AII |
| 61 | EEVDEDGSGT | IDFEEFLVM |
| 81 | VRQMKEDAKG | KSEEELADCF |
| 101 | RIFDKNADGF | IDIEELGEIL |
| 121 | RATGEHVTEE | DIEDLMKDSO |
| 141 | KNNDGRIDFD | EFLKMMEGVQ |
| 161 | | |

AMINO ACID SEQUENCE OF TROPONIN C
(EXCERPT FROM PDB)

SEQ ID NO: 5

Probe site = 81-108 in Calmodulin

[illegible]

rmsd = 0.567034



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Fig. 26

Probe site = 81-108 and 117-143 in Calmodulin

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----------------------------|
| 96 | 97 | 98 | 99 | 100 | 101 | 102 | 103 | 104 | 105 | 106 | 107 | 108 | 109 | 110 | SEQ ID NO: 6 < target > |
| L | A | D | C | F | R | I | F | D | K | N | A | D | G | F | |
| I | R | E | A | F | R | V | F | D | K | D | G | N | G | Y | SEQ ID NO: 7 < probe > |
| 111 | 112 | 113 | 114 | 115 | 116 | 117 | 118 | 119 | 120 | 121 | 122 | 123 | | | |
| I | D | I | E | E | L | G | E | I | L | R | A | T | | | SEQ ID NO: 6 < target > |
| I | S | A | A | E | L | R | H | V | M | T | N | L | | | SEQ ID NO: 7 < probe > |
| 132 | 133 | 134 | 135 | 136 | 137 | 138 | 139 | 140 | 141 | 142 | 143 | 144 | 145 | | |
| I | E | D | L | M | K | D | S | D | K | N | N | D | G | | SEQ ID NO: 8 < target > |
| V | D | E | M | I | R | E | A | N | I | D | G | D | G | | SEQ ID NO: 9 < probe > |
| 146 | 147 | 148 | 149 | 150 | 151 | 152 | 153 | 154 | 155 | 156 | 157 | 158 | | | |
| R | I | D | F | D | E | F | L | K | M | M | E | G | | | SEQ ID NO: 8 < target > |
| Q | V | N | Y | E | E | F | V | Q | M | M | T | A | | | SEQ ID NO: 9 < probe > |

rmsd = 0.823665

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Fig. 29

===== ATP/GTP binding site =====

Probe = (elongation factor)

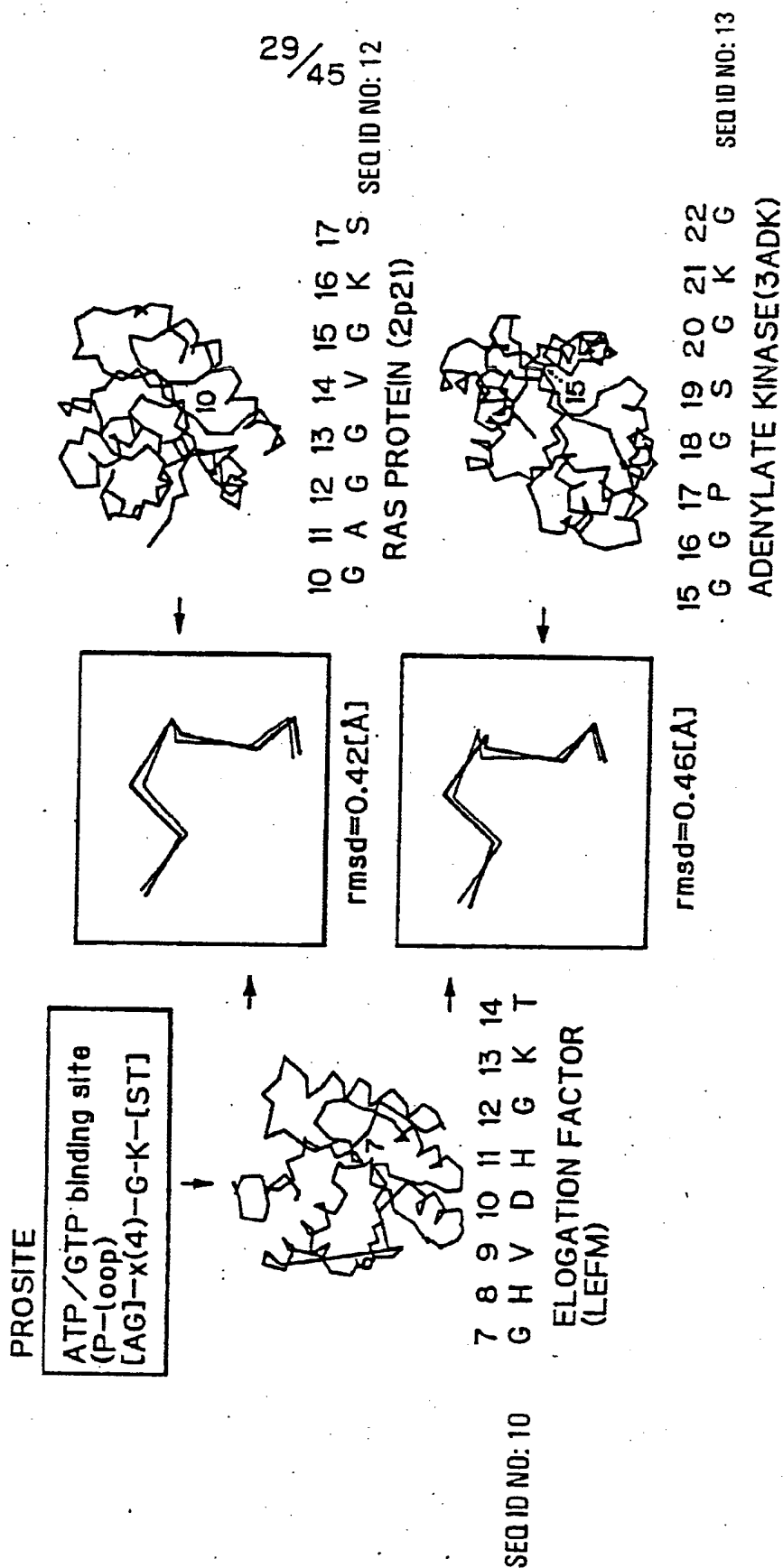
7 8 9 10 11 12 13 14
G H V D H G K T < probe > SEQ ID NO: 10

8 9 10 11 12 13 14 15
G A P G S G K G < target > SEQ ID NO: 11
G H V D H G K T < probe > SEQ ID NO: 10
rmsd=0.648732 adenylate kinase

unit - A

. : . : . :
10 11 12 13 14 15 16 17
G A G G V G K S < target > SEQ ID NO: 12
G H V D H G K T < probe > SEQ ID NO: 10
rmsd=0.421770 ras protein

Fig. 30



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Fig. 38 A

| | | | | | | | | | | | | | | | | | | | | |
|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | I | V | G | G | Y | T | C | C | A | N | T | V | P | Y | Q | V | S | L | N | S |
| 21 | G | Y | H | F | C | G | G | S | L | I | N | S | Q | W | V | V | S | A | A | H |
| 41 | C | Y | K | S | G | I | Q | V | R | L | G | E | D | N | I | N | V | V | E | G |
| 61 | N | E | Q | F | I | S | A | S | K | S | I | V | H | P | S | Y | N | S | N | T |
| 81 | L | N | N | D | I | M | L | I | K | L | K | S | A | A | S | L | N | S | R | V |
| 101 | A | S | I | S | L | P | T | S | C | A | S | A | G | T | Q | C | L | I | S | G |
| 121 | W | G | N | T | K | S | S | G | T | S | Y | P | D | V | L | K | C | L | K | A |
| 141 | P | I | L | S | D | S | S | C | K | S | A | Y | P | G | Q | I | T | S | N | M |
| 161 | F | C | A | G | Y | L | E | G | G | K | D | S | C | Q | G | D | S | G | G | P |
| 181 | V | V | C | S | G | K | L | Q | G | I | V | S | W | G | S | G | C | A | Q | K |
| 201 | N | K | P | G | V | Y | T | K | V | C | N | Y | V | S | W | I | K | Q | T | I |
| 221 | A | S | N | | | | | | | | | | | | | | | | | |

SEQ ID NO: 14

AMINO ACID SEQUENCE OF TRYPSIN (EXCERPT FROM PDB)

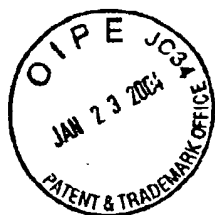
Fig. 38 B

| | | | | | | | | | | | | | | | | | | | | |
|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | V | V | G | G | T | E | A | Q | R | N | S | W | P | S | Q | I | S | L | Q | Y |
| 21 | R | S | G | S | S | W | A | H | T | C | G | G | T | L | I | R | Q | N | W | V |
| 41 | M | T | A | A | H | C | V | D | R | E | L | T | F | R | V | V | V | G | E | H |
| 61 | N | L | N | Q | N | N | G | T | E | Q | Y | V | G | V | Q | K | I | V | V | |
| 81 | P | Y | W | N | T | D | D | V | A | A | G | Y | D | I | A | L | L | R | L | A |
| 101 | Q | S | V | T | L | N | S | Y | V | Q | L | G | V | L | P | R | A | G | T | I |
| 121 | L | A | N | S | P | C | Y | I | T | T | G | W | G | L | T | R | T | N | G | Q |
| 141 | L | A | Q | T | L | Q | Q | A | Y | L | P | T | V | D | Y | A | I | C | S | S |
| 161 | S | S | Y | W | G | S | T | V | K | N | S | M | V | C | A | G | G | D | G | V |
| 181 | R | S | G | C | Q | G | D | S | G | G | P | L | H | C | L | V | N | G | Q | Y |
| 201 | A | V | H | G | V | T | S | F | V | S | R | L | G | C | N | V | T | R | K | P |
| 221 | T | V | F | T | R | V | S | A | Y | I | S | W | I | N | N | V | I | A | S | N |

SEQ ID NO: 15

AMINO ACID SEQUENCE OF ELASTASE (EXCERPT FROM PDB)

REPLACEMENT SHEET



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Fig. 39 A

Key site number 36 - 41 in Trypsin

| | | | | | | | |
|----|----|----|----|----|----|------------|---------------|
| 41 | 42 | 43 | 44 | 45 | 46 | | |
| M | T | A | A | H | C | < target > | SEQ ID NO: 16 |
| V | S | A | A | H | C | < probe > | SEQ ID NO: 17 |

$d = 12.070038$ [A]
 $r.m.s.d. = 0.061077$ [A]
 The number of atoms in a probe = 6
 The number of atoms in PDB = 240
 The number of combination = 1
 Time = 1sec

RETRIEVED RESULTS OF HISTIDINE ACTIVE SITES

Fig. 39 B

Key site number 175 - 179 in Trypsin

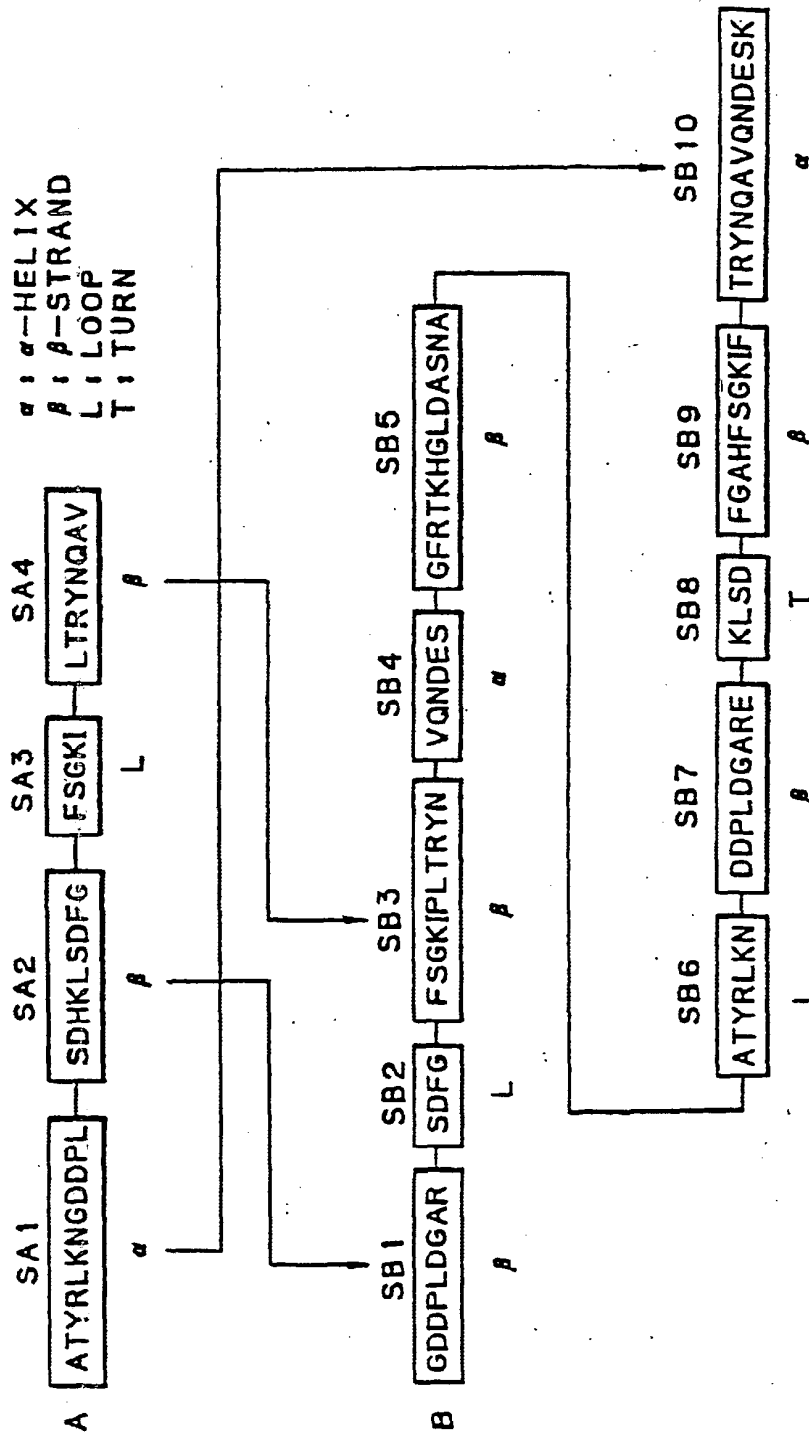
| | | | | | | |
|-----|-----|-----|-----|-----|------------|---------------|
| 186 | 187 | 188 | 189 | 190 | | |
| G | D | S | G | G | < target > | SEQ ID NO: 18 |
| G | D | S | G | G | < probe > | SEQ ID NO: 19 |

$d = 8.922721$ [A]
 $r.m.s.d. = 0.092879$ [A]
 The number of atoms in a probe = 5
 The number of atoms in PDB = 240
 The number of combination = 1
 Time = 1sec

RETRIEVED RESULTS OF SERINE ACTIVE SITES

A circular black ink stamp. The text "OIPE JC34" is curved along the top inner edge. The date "JAN 23 2004" is stamped in the center. The text "PATENT & TRADEMARK OFFICE" is curved along the bottom inner edge.

Fig. 46



SEQ ID NO: 20